

SEQUENCE LISTING



08/836,734

(1) GENERAL INFORMATION:

(i) APPLICANT: BECKMANN, JACQUES
RICHARD, ISABELLE

(ii) TITLE OF INVENTION: LGMD GENE CODING FOR A CALCIUM DEPENDENT
PROTEASE

(iii) NUMBER OF SEQUENCES: 67

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: NIXON & VANDERHYE P.C.
(B) STREET: 1100 NORTH GLEBE ROAD
(C) CITY: ARLINGTON
(D) STATE: VIRGINIA
(E) COUNTRY: U.S.A.
(F) ZIP: 22201-4714

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/836,734
(B) FILING DATE: 02-JUL-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: EP 94402668.1
(B) FILING DATE: 22-NOV-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: WILSON, MARY J.
(B) REGISTRATION NUMBER: 32,955
(C) REFERENCE/DOCKET NUMBER: 960-29

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (703) 816-4000
(B) TELEFAX: (703) 816-4100

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3018 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION: /label= FIGURE 8a

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

attorney: Segheto

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TGATAGGTGC TTGTAAACTG TGCTTAACGA AAACATACCG TGTGCTGTAG GGACTIONACT
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GGGTGACAGG AGTGAGAC

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (D) OTHER INFORMATION: /label= FIGURE 8b

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Sub
C1

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TAACTTTGCT TTTACAAAGT TGGTTTCATG TGTTCTTGAG CTTCTGTTC TCTCGTCTTC
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AGAGGCAATT CATTACTGAA TGAGCCATAA GCGCCTCTTA TTTCGAGAGG GGGATGGCAG
GACTCAGTCG AGGAGAAGGA CCGCACCCAG GCAGCCTGGG CCCCTCGGCT CCTGTACTTA
TTTACTGCTG GGTACTTCCT AGCCCAGCAT GTAATTACTG GTTCGTTGAG TCATTGTTTT
AGTAAATGTT TCTTGGGCAC CTACTACATA GGAGGCACAG GTCAAGGCAC TGGGGATATT
CTTTCTACCC ACCCCCTCCC TTGATACACT GTGATTAGGG ACTGACCGAT C

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: label= FIGURE 8c

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATTTTTTTTT TTTTTTTTGA GACGGAGTCT CACTCTGCCA CCCAGGCTGG AGTGCAATGG
CGCGATCTTG GCTCACTGCA ACCTCCGCCT CCCGGGTTC AAGTGATTCTT CTGCCTTAGC
CTCCTGAGTA GCTGAGACTA TAGGTGCCCC CCACCACGCC CAGCTAATTT TTGTATTTTT
ATTAGGACGG GGTTCACCA TATTGGCCAG GCTGGTCTCG AAATCCTGAC CTTGTGATCC
GCCCACCTCG GCCTCCCAA GTGCTGGGAT TACAGGTGTG AGCCATTGCG AGCAGCCCAG
AACTCAATTC TTAACCTTTA AAGTATGATG AGAAGAAGGA TCAAGCCCTC ACCAGCCCAT
TTAAGGAGTT TAGGCTCAGT CTTGAGGATG TGAGAAGTCA TTGCTATTGG GTTTCACACT
GAGGTTAACA GGTGAAGTCA GCATTTTGGT AGTTCACAGC AGCTGCAACT CTTTGTATTT
CTCTGATACC TCCTGTCCCA ACCTACATCA GGCCTTCCCT TCTTCCTGCT TCCTTAATTC
CTCCATTTTC CCACCAGATG GAAGGACTGG AGCTTTGTGG ACAAAGATGA GAAGGCCCCG
CTGCAGCACC AGGTCACTGA GGATGGAGAG TTCTGGTGAG TCCAGAACCC AGGAAGACCC
AGAAGGGTAA GGGTGGGGAA GAGAGGGGAA ATCTCAGACC TCAGTCCCCA GCTAAGGTAA
TCAGATTCCA GCCCTTGGGA GATCTTGGCT GTGTTCTCCT CCAGCCCAAG GCCCAGCAAG
GATGAGGTTT TGAGAGGAGC CTTCCAGGCC ACAGGGACAA TGAGCCCAGG ACCAGGCCAA
CATGACATGG CTCTTGCCCT CTGTGTGCCC CTCCGCCACA CACTCTATTC CAGCCACAGG

Sub
C1

CACCCTGGCC TTAGCACAAT TCTTTTCTGA GCCTAGGAAG CTCCACTTAC CCTGATCTTC
CAACGTCAAC CTCACCCTCT CTCAGGTTGT TTCTATTAG GCTTCAAGTC TCAGCTTAAG
GAGAATTTTC AAGTCTCAGC TTAAGGAGAG CCCCCTAAGT TCCCCGAGGA CTGGGATTAA
TTTATGATGC TCATCACCCCT TAAAATTGTT TGCTTAAGCC GGGCGCGGTG GCTCACGCCT
GTAATCCCGAG CACTTTGGGA GGCCGAGGTG AACGGATCAC GAGGTCAGGA GATCGAGAAC
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AACCTGGGAG GCAGAGGTTA CAGTGAGCCC AGATTGCGCC ACTGCACTCC AGCCTGGGCG
ACAAGAGAGA CTCTGTCTTG GAAAAAAAAA AAAAAATGTG GTCTTAGTTT AATGTCAAGG
GAAAGGTTTT GGGTGTTTTT ATTACTTTAT TTTTATTATA AAAACTATAA TAGAGACGGG
CCTCGCTATA TTTCTCGGGC TGGTCTCAAA CTCCTGGGCT CAAGCGGTCC TCCCACCTTG
GCCTCCCAA ATGCTGGCAT GTGGGCCTGG TCAACATATG GGACCCCAAC TCTACAAAAA
ATTTTAAAT TAGCCAGATG TGGTGGCGTG TGCTGTAGT CCCAGCTACT TGGGAGGCTG
AAGCAGGGGG TCACTTGAGC CCAGGAGGTT GAGGCTGCAG TGAACATGA TTGTCGTTCA
CTTTTCTTCT GAACGTGAGA TTAAGTGTA TCAGCAATTT GGCTTAGGAT TATTTATTCA
GAATTTTAA CCGTCACGTT GCGGCAAAACC AGGT

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (D) OTHER INFORMATION: /label= FIGURE 8d

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AGGAGGTGGA GGTGTCAGTG AGCCAAGATC ATGCCACTGC ACTCTAGCCT GGGCAACAGA
GCGAGACTCT GTCTCAAAAA ATACACACAC ACACACACAC ACACACACAC ACACACACAC
ACACACATAT ATATACACAC ATATATATAC ACACACATAT ACACACACAC ACGTCTGTAT
ATATATGTGT GTGTGTATAT ATACACACAC ACACTATTCT ATATATTCTT GTAGAGCTAT
GTGTGTCTCC TGTGCTATTG AGCATGAGCC CTTTTTTTTT TTTTTTTTTT TTGAGACAGA
GTCTCACTTT GTCGCCCAGG CTGGCATAACA ATGGCGCAAT ATCGGCTCAC TGCAACCTCC

Sub
C1

GCCTCCTGGG TTCAAGTGAT TCTCCTGCCT CAGCCTCCCA AGTAACTAGG ATTACAAGTG
CCCGCCATAA TGCTCAGCTA ATTTTGTAT TTTCAGTAGA GATGGGGTTT CACCATGTTG
GCCAAGCTGG TCTCAAACCTC CTAGCCTCAG GTGATCCACC TGCCTCAGCC TCCZAAAGTG
CTGGGATTAC AGGCATGAGC CACAGCACCC TGGTGAGCAC TAGAGCTTAT TTCTTCTATC
TAACTGTATT TTTGTATCCA TTAGCCACCC TCTTTTCATC CTCCCCTCTC CTTCCCTTCC
CAGCCTCTGG TAACCACTGT CTGCTCTCTA CTTCCATGAC ATATGCTTTG TTTTAGCTCT
CACATATGAG TGAGAGCATG CGACATTTAT CTTTCTGGCC CTGGCACATT TTTGAATCAT
TGTTAGAAAA GATGATGGTT TGGAGTAGAT ACATCAGAAG TGACAGCGTT TGCCCTAAAA
AGGAAAGACA GGCTCCTCTG GGACCCCTGAC CAAGTTCCTG TGAACATTTT TATTATTGTG
CTGTGTTAGT CCTGGGGTCT TCCGTTCCCA GCCCTCCTCA CCTGCTCCCA TATGGCTCTC
TCTCTTCTTC CAACCTCTCA GGATGTCCTA TGAGGATTTT ATCTACCATT TCACAAAGTT
GGAGATCTGC AACCTCACGG CCGATGCTCT GCAGTCTGAC AAGCTTCAGA CCTGGACAGT
GTCTGTGAAC GAGGGCCGCT GGGTACGGGG TTGCTCTGCC GGAGGCTGCC GCAACTTCCC
AGGTGGGAGA TGCTCTTGAT GGGGGGAGGG TCTAAGCCGA AAAAGTTCCA GGCAGAAGAA
GCCTAACTAG TGCTTATTAA GTCTCTCTGT TCCAGACGTC CACTATCTTA TTAAACCTTC
CCTGTTTTAC TGAGAAGGAA ACCACCATGC TGAGAAGTTT GCAATAGGGA GCTGGGTAGC
AACTTTGGAA GCAGGAACTT GTGGGAACAA TGCAGATGCT GCTTGGACTT ACGATGAGGT
TATGTCCAGA TAAGCCCATC CATCTTTTGA AAATACCCTA AGTGAAAAGT GCATCCAATA
TGCCTAACCC CCCAAACCTC ATAGCTTACC CTGGCCTACC CTCAAACATT GCTCGGAACC
CTTGACCTTA AGCCTAAAGT TGGGCCAAAT CATCTAACTC CAAAGCCTAT TTTACAAAGA
AAGTTGTTGT AATATCTOCA TGTAACCTTAC TTAATACTTG TACCTAAAAA GTGAAAAACA
AGAATGGTTG TACGGCTACT CGAAATCCAG TTTCTACTGA ATGTGCATCT CTTTCACATT
GTAAAGTTAA AAAATTGTAG CCGAACCATC CTAAGTCAGG GACTGTGAGT ACTGTGTCAG
TAACAGTAAG GGCACCTATT GAGAACCAAG TTAGCAGCTG CTGCAATAGT TCAAGTCAGA
GATGATGAAA ACCTAGACCA AGTCAGTAGC AGCAGAGATG GAGGGGAGAC AGCAGATTTA
GGGAGAGCAT ATTGGGTGAT GTAGGGAAGG AAGAAGAATG ATGTCAAGAT TCCCAGTTGG
GGACCTGACA ACATTGCAAC ATAAGACACA CAAGAAGATC GGGTGGGTGG CTCATGCCTA
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CAGCAGAGGC AACATAGTGA CACCTCATCG TTACCCAAAA TAAAAAATAA AATGAGGTGG
GAGGATTGCT TGAGCTCGGG AGGTTGAGGC TACAATAAAC TGTGATCATG CCACTGCACT
CCTGCCTGGG TGACAGAGTG AGACCCTGCC TCAAAAAAAA AAGACACACA AGAGAAAAAT

Sub
C1

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CTTGGGACAT GGAAAGTTTG AGGTTCTGT AGAGTGTCCT AGTGAAGATT TGTAAATAGAG
CATCGGATGC GCATATTAGA TGGCACTTGG TGATATGATA AGAACTCAAA AAATATTTGA
GGAATAAAGG AAAGAAGAGG CCAGACGTGG TGGCTTATGC CTGTAATCCC AGCACTTTGG
GAGGCTGAGG CAGGCGGATC ACTTGTGGTC AGGAGTTCGA GACCAGCTTG GCTAACATGG
TGAAAACCCA TCTCTACTAA AGATACAAAA ATTAACCGGG GATGATGGTG GGTGCCTGTA
ATCCCAGCTA CTTGGGAGGC TCAGTCAGAA GAATCGCTTG AACCCAGGAG GCGGAGGCTG
CAGTGAGCCG AGATCGCGCC ACTGCACTCT AGCCTGGGCA ACAGAGCCAG ACTCCGTCTC
AAAAAAAAA AAGTGAGAGA GATTGAGGCT GGGATATATG GCTCAGGCAT CATGCGCGTG
TAGGGGGCAG TTA AAAAGCA GAAGTAAGAA AGATTGCCTA GGGAGGCAGG AAGGGTGAGG
TGAGAGGAGA AGAGGCCAG GACCAGATTC TAGTCACCAA CAGCGTTTAA GGGGCAGGTA
AGGAAAACAA AACCATCAGC AAAGACTGAG AATGAAAGCC CAGAGAGGAA GGAAAAGCCA
CACATACAAT CAGTACAGCT CCATCTGAAT AAAGGTAGCG CCCCCCCCCC CCCAATCAT
TAGAGAAATG CCTGATTGCG TTTTCTGTGG ATTTTTCCTA AGAACCTAGA TGTGGGGAAT
AGAAATAAAT GGTTCCTCT GTCTCATCCC CTCCCTGCCC TCTGAGAGGA AGCTGTGATT
GCGTGCTCCC TTTCTGGGGG TGCAGATACT TTCTGGACCA ACCCTCAGTA CCGTCCGAAG
CTCCTGGAGG AGGACGATCA CCCTGATGAC TCGGAGGTGA TTTGCAGCTT CCTGGTGGCC
CTGATGCAGA AGAACCGGCG GAAGGACCGG AAGCTAGGGG CCAGTCTCTT CACCATTGCC
TTCGCCATCT ACGAGGTGTG TAGTCCTGAT TGGCTCCAGC CCAGGAAACA TACTTTCCCA
GAGAGGACGC TTCCAGGGGC TTCTAGAGGG GCCCTCTGCT TCCTCAATAC CAGTGACCCA
CAGAGCTCCT GGTATCAGGA CCACTTGTGT TTGTAACAAG CAAAAAATAC CAGGGGGGGC
ATTAGAGAGG CAGTGGAGCG GGCCTGGCAG AACAGGTGCC TGGGGGTCAG GCTTCCGCAT
GCGGGCTCCA GTTGCTGGCA TTGCCTTCCG CAGGCTCCTC ATCCTCATTC ACATCTGAAG
CATCTTCCTT TCTGTTTCTT CTCAAGGTTT CCAAAGAGGT ATAGCAGCAG CAGCGGCCAG
CAGTTGTGTG CAGCACTACC CAGGGGGGCC CGAGTCTGTC TGTGGCTCGT CGAGAAGCTT
CCTGGTGGGG TTTGTGGGCA GGA CTGTGTA TAGGAGAGGG CCTTGCCTGT TGTATTTC
CACTTGCAGA GCAGGTTGCC TCAGGGCATT GCATGACCCA TGACTACCAC CCCCAGGATG
TGCACTTTCT CCCTCGCACC AGACACTGCA CGTCACACAC ATGCCTTTGC AACTCACCC
TCCTCCACGC TTACAGCCAC ACACACAGTC ACACAGACGC GTTCTGAGGG TGGCTGCCCC
CTTGGGATGG AGGAATCACT TCCCTCAGAA CCCAGCCAAG TCCTCTAGGC CTCCTTGGGG

Sub
C1

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TGTGGGGATG ACACATTTCC ATTCACCTCTG AATCACAACA GAAAAGGGAA GAGGAATTGA
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GGTGACCAGG GAGTTGGGAA GGGACCCTTG GAGGTGGCTG TGGCAGGACA GGACGTTCTT
CCCGAGGGGC TCATGTGCCC TGGGCTCTCC CCATCTCTCA GATGCACGGG AACAAGCAGC
ACCTGCAGAA GGACTTCTTC CTGTACAACG CCTCCAAGGC CAGGAGCAAA ACCTACATCA
ACATGCGGGA GGTGTCCCAG CGCTTCCGCC TGCCTCCCAG CGAGTACGTC ATCGTGCCCT
CCACCTACGA GCCCCACCAG GAGGGGGAAT TCATCCTCCG GGTCTTCTCT GAAAAGAGGA
ACCTCTCTGA GTGAGTGCTG GCCCAGCTTT CCCACGTGTT TCTAAAAGCT CACATGGCCC
ACTCCAGAGG TTGAAGGCAT GAGGCAGCTA GACACGTCTC CTCCAGGGTC CTTCTGCTGC
TCCTGAGCCA CTGGCCACAT TACCCCCATT CATTCAATTCA TCCATTCTGT GATATTTATT
GAGCACCTAC TATGTTCCAG GCACTGTCCT AGGCACTAAG GATAGAGTAG TGAAGTAAAC
AGAAAGAAAT CCCTGCCTTC ATGGAGCTTA ATATTCTAAC ATGAGACAAT AATGGATAGG
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AGAGGGATAG GAGGTGTTGG GGATGCTTGA AATTTTAGGT TAGCATGGCC AGGAAAGCCA
CATCCTGTCC CTGGCCACCA CAGATGAGCT CATAGCCCCT GCCACTCTGA TCTCTGTCTT
TGGAAGATGC ACCAGGTCCA TGGTAGGTG GCTGGGTCAT GCCTTTGGGG GGCTCTGAGC
AATACTAACA AGAACCTGCG TGCCTGGGCT TGGCTGTCGG GGATGGTGCT GACATGGGGC
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AGACCCACA TGTCTGTATT CCTCACAGGG AAGTTGAAAA TACCATCTCC GTGGATCGGC
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CTGGAAAGGA GAAGCAATTT GAACAATCGG AGGGAACAAG GCCACAGGAA GGGATGACAA
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ATAATGTGCC TTGCAAGGCT TTTGTGAGGC TTCATCAATG AGGTGATGTA TGTGAAGTGT
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Sub
C1

CTTTTCACAT GTGTCATCGC GATACTTGCA AGGTTGCTGA GAGGTAGATG GGGTTATAAT
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CAGAGCTCAG TAAGTGGCAG GGTTTGGAAC TCACATTCAG ACTCTCTGAC TCCAGACTTA
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GCACAGAGTG CTGTGTGTTG GGCTCTGTGT GTTGAGGAGT CTTGTGACTG CCTTGGGGCT
TTGGGCTGTA GTCAGCTGAC AGTCCTTTGT GCTCTGTGGG GATGACGTAG GCCAATGGGA
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GTAGGTGCGT GGGGATCTGT TCTGGTCATC TGGATGCTGG TCATCGGGTG CAGTATTGAT
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GTGCAGGGTT TTTGATGTCC CTGCACTGAC ACAGTTGTCT GCAGTTCTCC AATTTGACAT
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ACACAGGGAG CAGGGCCCTT TGGCTCAAGC TGATAGTTGC CGCAGGGATT ACCAGGCCCA
GGGCAGCCTG CCACAAGCTG GGGCTTTTAC CAAAGAAAAT CTCCTATGT TAAATGCTTG
CTCAAAAATT TTTAAAAAAT ATTCTGTAAG TCAAAATCCA TTGTTAGGTC AGTTTGAGAG
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CAGACTTGCC TCTTCTCCC CCTCCTTCTT GAGCTTCTGC TGGGGCCGAG CGTGCAGTAA
TGACAACTAC GATTTGCTGG GGAAGGCTA CGTGCCAAGC ACTCTTTTAG GTGCTTTCCA

sub
C1

TGATTAATTC CTTCTCACA ACAGCCCTAT GAGATTAGTA CTATAACTAT CCCCATTTC
AGAGGGAGAA AAGGTACAGA CTTGACTAAC TTGCCAAGG CCACACAGCC AGAGAGGGG
AGAGCCAGTA CTTAGAGCCA GGCAGTCTGG GTCCAGAGTC CGTGTCTGA ACCACAAGAG
GCCATCATAC GCCATCAGAT TTGGTGCTAG CATTCTGGT GGTGCCTGGT GGTGATGGAT
CCATCACAGG GGTCTCCAG GTACTGGTGC TGGCCAGAC CAGAGCTGAC ACTCCTCAGG
CACTACCACA TTCCAGGCAC TGTGCTTGGG GTCAGTCCCT CTCTTTTTT TCCCCCAA
TTATAACAGT ATCTACAAAG TAGGTGCTGT TATTTTTCCC CTTTCACAGG TGAGATAGAC
TCAAAGAAGT GAACTGCCC AAGGAACAGA ACTAATGAGT GGGGAAAATG GAACTGGAAA
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GCAAGCCAAG GCCTCTGGGG CCTGCTGGGA GCGAAAGCTG GGGAGCCGTT TCCACGGGTC
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ATGGTCTTGA TCTCCTGACC TTGTGATCTG CCTGCTTCGG CCTCCTAAAG TGCTGGGATT
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TTTCACGTGC TGAGCTCTCA ATACTCTACC ATGAGGAGGG ATGGAGTGGG TATGAAAAGA

Sub
C1

TAAAGAACTG AAGTCACACG GCTTGTCACT GGCAGAGATA GAGCTTGAAC CGAGGTTGAA
GAGCTCCCGC CTATTCCTTT CCTCTTCTCA CTGGATAAAG CTGCTCCAAG AGAGGTGCTG
CCTCAGTGTG CCTGTTTACA CTGTAATCCT CCCTTCCTTC CTGCCTCCTC CCTCCTCTCT
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GGAGTCAGAG GAGGGCAAAG GCAAAACAAG CCCTGATAAG CAAAAGCAGT CCCCACAGGT
GTCTGGGCAT GTGGCATGGG TGGGGTGGCC AGCACGCTAC AGGGGCTTCC TATGCGCTTG
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TGTCCCACTG ACCTTTTCTT TCAGCAAGTT CCCCTGAAAT TTGGGCTGCT GCTTGGGTGA
ATATCCCAGG ATGGGGGTTT CATTCTAGGA GTGGACTGGC AGGCTGAGCC TCCCATGGAG
CTGATCCAGC CAGGATACAG AGAAGGGGAG GCAAAGGCTG AGACAGAACC AGCTTGAGAG
CGGAGGCGCA ACTCTTGTCT CCTGGTGGCC TTGAGCATTT CACAATAGGG GGATAAAGGA
TAGGAGCAGA AAAGTGGGGC TGACTTCAGA AATGGGGTCC TCTAGAGCTC ACGGGAGGGT
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GCACCTTTAG TTGGAATGCT CAGGCCTGGG ATGGTGGAGG GGGCTCTTGC AGGTGGGGAC
TGGGGTGGCG GGGAGGAGGC TGTATGGCCG CCATATCTCC TTTGGCTGGG GCGCTCAGGG
CTGGAGAGGT GTGAAGAGTC CCTGAGGCCT CGATGCATCT CACTCCAGCT CACCAGGTCT
GCATTTGCCC GTCCCGAGCT CCTGCTGCCA CCCCCGCCG TTTAGGCAC TTGGCTCCCT
TGGCCAGAG GAGCTTGCCT CACAGGCCTG TGCACCTCTG ACCCCTGTGA ACCAGTTTTC
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ATTCCGGAAC ATTTTCAAGC AGATAGCAGG AGATGTGAGT ACCTCCAAGC CCAGGACGCC
CACAGGTGCT TCCTTCTCTC CTGGATTAAC TGCTCAGATT ACCAATTATT TCATTATTGT
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TGAGCTGCCC ACGGTGGTCC TGATAGCTGA GGTGCAGTAT CTGGCCCCCT GTCTTCCTCA
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TCCTCTCCCT TCCTCTCAG GACATGGAGA TCTGTGCAGA TGAGCTCAAG AAGGTCCTTA

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GGCCTGGCAG GTGGGAAGAG AAAATGAAGC GTGGGAGTCA AGAATGGGGT TGATTTGGAG
ATTGAGTGTG TGACCTCCAT CCTCAAATTT TCTATTGCCA GAAAATTTTC AAACACTATG
ACACAGACCA GTCCGGCACC ATCAACAGCT ACGAGATGCG AAATGCAGTC AACGACGCAG
GTGCTGAGAA GGAAGGGGTG TCAGGGATGT GGACCCGAGA CGGTGGGAGC AGGAATGGGA
GGGGACTAGC TACTAGGGCC CCACTAGAGA AGGAGAGGGA AAGGGCTTCT CACTTTCCCT
TCCCAGGTCA CAGAGTGTCC GAGAGGCAGG GAAAATAGAA GACAGGCCCA AGGCCTCCAG
CTCCACGTCC ACCTCTAACA TGGTCCCTC CACAGGATTC CACCTCAACA ACCAGCTCTA
TGACATCATT ACCATGCGGT ACGCAGACAA ACACATGAAC ATCGACTTTG ACAGTTTCAT
CTGCTGCTTC GTTAGGCTGG AGGGCATGTT CAGTAAGTGG GAGAGGGGGG CTGCCCTCTG
CTCTCTTGCA GGGGCAGTTG TGGCAACAGG CATCTCACCT GATAATCTCC AGTCTGCTCC
ATCCAGGCTG AACGAGGGCC AATGACCTCT TTAGGCCCAG AATGGGATGG CAAAGGGAGG
GTTACTGGTG ATTCTCTGCC TGCACATCTT TGTGCTGATG AGGGACAGCA CTGGGCACAC
GGTCTCTGA GGGGAAGTTA CAGTAGTAGA GGCGGAGTGC GCCTGTAACT GGCCTCTGGC
CTGTGCATT TTTACAGGA GCTTCTCATG CATTTGACAA GGATGGAGAT GGTATCATCA
AGCTCAAGCT TCTGGAGGTA AAGCATAGGC ACAGCACATT CCCCCTACAC ATTAAACTC
AAGGTGGAGG GGTCAACGGG GCGGACTGGA CCCAGGGTGT GCTCCTCATT TCCACACAGT
GGTGGAGGGA AGGGATAGGA ACAGAACATG GAGGGAGGCT CAGCAGGCTC CCAGGACACA
TGCCTTGAG GCCAAAAGG ACCTCTGCTC CCCAGTCAC TTGATGCGGG AAAACATGCA
CCTTCTTAGG GAAGATCTAG GAGAAAGGAA ACAGTAAGCC ACTGCTTCTT GGAAAATCTT
CTGGGGTCT GACCTGCTGG GACTGTTCCC TTTCTCTTG CCCCCTAAGA TTCCTAGGGC

Sub
C1

Sub
C1

GGGGGGGGGG GGGGGTCACT CTTTCTGAT CTACATTCTG ATCTTGGGAC TTCTTTCACT
GGCTGCAGCT CACCATGTAT GCCTGAACCA GGCTGGCCTC ATCCAAAGCC ATGCAGGATC
ACTCAGGATT TCAGTTTCAC CCTCTATTTC CAAAGCCATT TACCTCAAAG GAQCCAGCAG
CTACACCCCT ACAGGCTTCC AGGCACCTCA TCAGTCATGT TCCTCCTCCA TTTTACCCCC
TACCCATCCT TGATCGGTCA TGCCTAGCCT GACCCTTTAG TAAAGCAATG AGGTAGGAAG
AACAAACCCT TGTCCCTTTG CCATGTGGAG GAAAGTGCCT GCCTCTGGTC CGAGCCGCCT
CGGTTCTGAA GCGAGTGCTC CTGCTTACCT TGCTCTAGGC TGTCTGCAGA AGCACCTGCC
GGTGGCACTC AGCACCTCCT TGTGCTAGAG CCCTCCATCA CCTTCACGCT GTCCCACCAT
GGGCCAGGAA CCAAACCAGC ACTGGGTTCT ACTGCTGTGG GGTAAACTAA CTCAGTGGAA
TAGGGCTGGT TACTTTGGGC TGTCCAATC ATAAGTTTGG CTGCATTTTG AAAAAAGCTG
ATCTAAATAA AGGCATGTGT ATGGCTGGTC CCCTTGTGTT TTGTTGTCTC ACATTTAGAT
ATCAGCCATG CATGACTGAA TGGCTTCCAA TCATATACTC ACCTATCACC TACAAGAGAA
CAATGAAAAA CACACACAAA AACAAAATCT TGAATTTTGT AATCATGCCT ATTGCTATTT
CTTGAGCATA AGAATGGCTC AGATACTTTC CAAGACATAA AAGGAAGGCA GAGGAATAGT
TGTTGCTGTA AAAGACATCA AGAATAAATG GGGTCATGTA CAACGGGAGG GGCCGGTTAC
CTGAATAATG GAGTGGAGAT TGAGCTATCC TAGCTCCTCT GCTCACTAAC TGACCTGTGC
CATGACCGTG GACAAAACCC TGACGCGAGC TGTTTGTTTG CTAAACTTCT CTGGACCATG
GCCTGCGGCA TATCTATAGG CATCCTGTGT TTTCCACCCA GTTTCCTTCT TCCTCGCTAA
GCCAACGTGG AAAGGGCTGG CCGTGAATAT GCAGACAAGG TAACGAAAGT AAACCGTCAA
TTAGTAAAAG TACTTCATTT TCCTCTTGTA TTTGCTTCAT TCTTGCTTCA CAAAGTTACG
AAGTCCACAG CTTTATACCA AAATGTAAGA AGGCTATTTG CTTATAAACA TTTTGAGTCA
GGTGTCATCT GATTTTATTC TTCTAATCCA TATTCAATAT TAAAAAATCA GAAACCAAGG
GTGCTGGAGC AGCTCTAGGG CATATATTTT TCTTAAATAG GAGAAAGATT TTCAACAGCT
TTTCCTCCTT GACCCCTCC TTTCCCAATT TATTGGGTC ACTACCTTGA ATTTAGAGTG
AATCTGGGAA ATGTAGTCAC CAGG

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= FIGURE 2

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) POSITION : 1303..3764
(D) OTHER INFORMATION:/note=CDS

Sub
C1
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) POSITION : 1631
(D) OTHER INFORMATION:/note= CGA->TGA ; nCL1 mutation in one
LGMD2A family

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) POSITION : 1848
(D) OTHER INFORMATION:/note= CTG->CAG ; nCL1 mutation in one
LGMD2A family

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) POSITION : 1853
(D) OTHER INFORMATION:/note= CAA->CA ; nCL1 mutation in one
LGMD2A family

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) POSITION : 2004
(D) OTHER INFORMATION:/note= GGG->GAG ; nCL1 mutation in one
LGMD2A family

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) POSITION : 2248
(D) OTHER INFORMATION:/note= CGG->CG ; nCL1 mutation in one
LGMD2A family

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) POSITION : 2364
(D) OTHER INFORMATION:/note= GTG->GGG ; nCL1 mutation in one
LGMD2A family

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) POSITION : 2382
(D) OTHER INFORMATION:/note= TGG->TAG ; nCL1 mutation in one
LGMD2A family

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) POSITION : 2771
(D) OTHER INFORMATION:/note= CGG->TGG ; nCL1 mutation in one
LGMD2A family

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) POSITION : 3018

(D) OTHER INFORMATION:/note= GGG->CAG ; nCL1 mutation in one
LGMD2A family

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) POSITION : 3372..3373

(D) OTHER INFORMATION:/note= Deletion AC ; nCL1 mutation in

one

LGMD2A family

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) POSITION : 3533

(D) OTHER INFORMATION:/note= AGC->GGC ; nCL1 mutation in one

LGMD2A family

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) POSITION : 3609

(D) OTHER INFORMATION:/note= CGG->CAG ; nCL1 mutation in one

LGMD2A family

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) POSITION : 3616..3619

(D) OTHER INFORMATION:/note= Deletion AGAC ; nCL1 mutation in

one

LGMD2A family

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) POSITION : 3665..3666

(D) OTHER INFORMATION:/note= AG->TCATCT ; nCL1 mutation in one

LGMD2A family

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATATCAGTTA GCCTGGTTTC ACTATACAGT ACATCATTTT GCTTAAAGTC ACAGCTTACG
AGAACCTATC GATGATGTTA AGTGAGGATT TTCTCTGCTC AGGTGCACTT TTTTTTTTTT
TTAAGACGGA GTCTCTTTCT GTCACCTGGG CTGGAGTGCA GTGGCGTGAT CTGGGTTCAC
TACAACCTCT CCTCCTGGG TTCAAGCAAT TCTTCTGTCT CAGCCTCCCA AGTAGCTGGG
ATTACAGGCA CCCCCCGCCA CACCCGGGCTT ATTTTGTAT TTTTAGTAGA GACAGGGTTT
CACTATTGTT GTCCATGCTG GTCTCGAACT CGTGACCTCA TGTGATCCAC CCGCCTCGGC
CTCCCAAAGT GCAGAGATTA GAGACGTGAT CCACATGGCC CAGCAGGACC ACTTTTTAGC
AGATTGAGTC CCAGTGTTCA TTTTGTGGAT GGGGAGAGAC AAGAGGTGGC AAGGTCAAGT
GTGCAGGTAG AGACAGGGAT TTTCTCAAT GAGGACTCTG CTGAGTAGCA TTTTCCATGC
AGACATTTCC AATGAGCGCT GACCCAAGAA CATTCTAAAA AAGATACCAA ATCTAACATT
GAATAATGTT CTGATATCCT AAAATTTTAG GACTAAAAAT CATGTTCTCT AAAATTCACA

GAATATTTTT GTAGAATTCA GTACCTCCCG TTCACCCTAA CTAGCTTTTT TGCAATATTG
TTTTCCATT CATTGATGGC CAGTAGTTGG GTGGTCTGTA TAACTGCCTA CTCAATAACA
TGTCAGCAGT TCTCAGCTTC TTTCCAGTGT TCACCTTACT CAGATACTCC CTTTTCATTT
TCTGGCAACA CCAGCACTTC ATGGCAACAG AAATGTCCCT AGCCAGGTTC TCTCTCTACC
ATGCAGTCTC TCTTGCTCTC ATACTCACAG TGTTTCTTCA CATCTATTTT TAGTTTTCTT
GGCTCAAGCA TCTTCAGGCC ACTGAAACAC AACCCTCACT CTCTTCTCT CTCCCTCTGG
CATGCATGCT GCTGGTAGGA GACCCCAAG TCAACATTGC TTCAGAAATC CTTTAGCACT
CATTTCTCAG GAGAACTTAT GGCTTCAGAA TCACAGCTCG GTTTTTAAGA TGGACATAAC
CTGTCCGACC TTCTGATGGG CTTTCAACTT TGAAGTGGAT GTGGACACTT TTCTCTCAGA
TGACAGAATT ACTCCAACTT CCCCTTTGCA GTTGCTTCCT TTCCTTGAAG GTAGCTGTAT
CTTATTTTCT TTA AAAAGCT TTTTCTTCCA AAGCCACTTG CCATGCCGAC CGTCATTAGC
GCATCTGTGG CTCCAAGGAC AGCGGCTGAG CCCCAGTCCC CAGGGCCAGT TCCTACCCG
GCCCAGAGCA AGGCCACTGA GGCTGGGGGT GGAAACCCAA GTGGCATCTA TTCAGCCATC
ATCAGCCGCA ATTTTCCTAT TATCGGAGTG AAAGAGAAGA CATTGAGCA ACTTCACAAG
AAATGTCTAG AAAAGAAAGT TCTTTATGTG GACCCTGAGT TCCCACCGGA TGAGACCTCT
CTCTTTTATA GCCAGAAGTT CCCCATCCAG TTCGTCTGGA AGAGACCTCC GGAAATTTG
GAGAATCCCC GATTTATCAT TGATGGAGCC AACAGAACTG ACATCTGTCA AGGAGAGCTA
GGGGACTGCT GGTTCCTCGC AGCCATTGCC TGCCTGACCC TGAACCAGCA CCTTCTTTTC
CGAGTCATAC CCCATGATCA AAGTTTCATC GAAAACTACG CAGGGATCTT CCACTTCCAG
TTCTGGCGCT ATGGAGAGTG GGTGGACGTG GTTATAGATG ACTGCCTGCC AACGTACAAC
AATCAACTGG TTTTCACCAA GTCCAACCAC CGCAATGAGT TCTGGAGTGC TCTGCTGGAG
AAGGCTTATG CTAAGCTCCA TGGTTCCTAC GAAGCTCTGA AAGGTGGGAA CACCACAGAG
GCCATGGAGG ACTTCACAGG AGGGGTGGCA GAGTTTTTTG AGATCAGGGA TGCTCCTAGT
GACATGTACA AGATCATGAA GAAAGCCATC GAGAGAGGCT CCCTCATGGG CTGCTCCATT
GATGATGGCA CGAACATGAC CTATGGAACC TCTCCTCTG GTCTGAACAT GGGGGAGTTG
ATTGCACGGA TGGAAGGAA TATGGATAAC TCACTGCTCC AGGACTCAGA CCTCGACCCC
AGAGGCTCAG ATGAAAGACC GACCCGGACA ATCATTCGGG TTCAGTATGA GACAAGAATG
GCCTGCGGGC TGGTCAGAGG TCACGCCTAC TCTGTCACGG GGCTGGATGA GGTCCCGTTC
AAAGGTGAGA AAGTGAAGCT GGTGCGGCTG CGGAATCCGT GGGGCCAGGT GGAGTGGAAC
GGTTCTTGGA GTGATAGATG GAAGGACTGG AGCTTTGTGG ACAAAGATGA GAAGGCCCGT

Sub
C1

CTGCAGCACC AGGTCACTGA GGATGGAGAG TTCTGGATGT CCTATGAGGA TTTCATCTAC
CATTTACAA AGTTGGAGAT CTGCAACCTC ACGGCCGATG CTCTGCAGTC TGACAGCTT
CAGACCTGGA CAGTGTCTGT GAACGAGGGC CGCTGGGTAC GGGGTTGCTC TGCCGGAGGC
TGCCGCAACT TCCCAGATAC TTTCTGGACC AACCTCAGT ACCGTCTGAA GCTCCTGGAG
GAGGACGATG ACCCTGATGA CTCGGAGGTG ATTTGCAGCT TCCTGGTGCC CCTGATGCAG
AAGAACCGGC GGAAGGACCG GAAGCTAGGG GCCAGTCTCT TCACCATTTG CTTGCCCATC
TACGAGGTTT CCAAAGAGAT GCACGGGAAC AAGCAGCACC TGCAGAAGGA CTTCTTCTG
TACAACGCCT CCAAGGCCAG GAGCAAAACC TACATCAACA TCGGGGAGGT GTCCCAGCGC
TTCCGCCTGC CTCCCAGCGA GTACGTCATC GTGCCCTCCA CCTACGAGCC CCACCAGGAG
GGGAATTCA TCCTCCGGGT CTTCTCTGAA AAGAGGAACC TCTCTGAGGA AGTTGAAAAT
ACCATCTCCG TGGATCGGCC AGTGAAAAAG AAAAAACCA AGCCATCAT CTTCGTTTCG
GACAGAGCAA ACAGCAACAA GGAGCTGGGT GTGACCAGG AGTCAGAGGA GGGCAAAGGC
AAAACAAGCC CTGATAAGCA AAAGCAGTCC CCACAGCCAC AGCCTGGCAG CTCTGATCAG
GAAAGTGAGG AACAGCAACA ATTCCGGAAC ATTTTCAAGC AGATAGCAGG AGATGACATG
GAGATCTGTG CAGATGAGCT CAAGAAGTTC CTTAACACAG TCGTGAACA ACACAAGGAC
CTGAAGACAC ACGGGTTCAC ACTGAGTCC TGCCGTAGCA TGATTGCGCT CATGGATACA
GATGGCTCTG GAAAGCTCAA CTTGCAGGAG TTCCACCACC TCTGGAACAA GATTAAGGCC
TGGCAGAAAA TTTTCAAACA CTATGACACA GACCAGTCCG GCACCATCAA CAGCTACGAG
ATGCGAAATG CAGTCAACGA CGCAGGATTC CACCTCAACA ACCAGCTCTA TGACATCATT
ACCATGCGGT ACGCAGACAA ACACATGAAC ATCGACTTTG ACAGTTTCAT CTGCTGCTTC
GTTAGGCTGG AGGGCATGTT CAGAGCTTTT CATGCATTTG ACAAGGATGG AGATGGTATC
ATCAAGCTCA ACCTTCTGGA GTGGCTGCAG CTCACCATGT ATGCCTGAAC CAGGCTGGCC
TCATCCAAAG CCATGCAGGA TCACTCAGGA TTTCAGTTTC ACCCTCTATT TCCAAAGCCA
TTTACCTCAA AGGACCCAGC AGCTACACCC CTACAGGCTT CCAGGCACCT CATCAGTCAT
GTTCTCTCTC CATTTTACCC CCTACCCATC CTTGATCGGT CATGCCTAGC CTGACCCTTT
AGTAAACCAA TGAGGTAGGA AGAACAACCC CTTGTCCCTT TGCCATGTGG AGGAAAGTGC
CTGCTCTGG TCCGAGCCGC CTCGGTTCTG AAGCGAGTGC TCCTGCTTAC CTTGCTCTAG
GCTGCTGCA GAAGCACCTG CCGGTGGCAC TCAGCACCTC CTTGTGCTAG AGCCCTCCAT
CACCTTCACG CTGTCCACC ATGGGCCAGG AACCAAACCA GCCTGGGTT CTA CTGCTGT
GGGTAAACT AACTCAGTGG AATAGGGCTG GTTACTTTGG GCTGTCCAAC TCATAAGTTT
GGCTGCATTT TGAAAAAGC TGATCTAAAT AAAGGCATGT GTATGGCTGG TCCCCTTGTG

TTTTGTTGTC TCACATTTAG ATATCAGCCA TGCATGACTG AATGGCTTCC AATCATATAC
TCACCTATCA CCTACAAGAG AACAAATGAAA AACACACACA AAAACAAAAT CTTGATTTT
GTAATCATGC CTATTGCTAT TTCTTGAGCA TAAGAATGGC TCAGATACTT TCCAAGACAT
AAAAGGAAGG CAGAGGAATA GTTGTGCTG TAAAAGACAT CAAGAATAAA TGGGTCATGT
ACAACGGGAG GGGCCGGTTA CCTGAATAAT GGAGTGGAGA TTGAGCTATC CTAGCTCCTC
TGCTCACTAA CTGACCTGTC GCATGACCGT GGACAAAACC CTGAACGCAG CTGTTTGTTT
GCTAAACTTC TCTGGACCAT GGCCTGCGGC ATATCTATAG GCATCCTGTG TTTTCCACCC
AGTTTCCTTC TTCCTCGCTA AGCCAACGTG GAAAGGGCTG GCCGTGAATA TGCAGACAAG
GTAACGAAAG TAAACCGTCA ATTAGTAAAA GTACTTCATT TTCCTCTTGT ATTTGCTTCA
TATCTTGCTT CACAAAGTTA CGAAGTTCAC AGCTTTATAC CAAAATGTAA GAAGGCTATT
TGCTTATAAA CATTTTTGCA GTCAGGTGTC ATCTGATTTT ATTCTTCTAA TCCATATTCA
ATATTANAAA AATCAGAAAC CAAGGGTGCT GGAGCAGCTC TAGGGCATAT ATTTCTCTTA
AATAGGAGAA AGATTTTCAA CAGCTTTTCC TCCTTGACCC CCTCCTTTCC CAATTTATTT
GGGTCACTAC CTTGAATTTA GAGTGAATCT GGGAAATGTA GTCACCAGG

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc-feature
- (D) OTHER INFORMATION:/label= "FIGURE 2"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:1..61
- (D) OTHER INFORMATION:/label= ALU
/note= "FIGURE 3 - HUMAN"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:268..309
- (D) OTHER INFORMATION:/label= ALU
/note= "FIGURE 3 - HUMAN"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:310..328
- (D) OTHER INFORMATION:/label= ALU
/note= "FIGURE 3 - HUMAN"

(ix) FEATURE:

(A) NAME/KEY: Region
(B) LOCATION: 578..618
(D) OTHER INFORMATION: /label= ALU
/note= "FIGURE 3 - HUMAN"

(ix) FEATURE:

(A) NAME/KEY: Region
(B) LOCATION: 619..653
(D) OTHER INFORMATION: /label= ALU
/note= "FIGURE 3 - HUMAN"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Pro Thr Val Ile Ser Ala Ser Val Ala Pro Arg Thr Ala Ala Glu
1 5 10 15
Pro Arg Ser Pro Gly Pro Val Pro His Pro Ala Gln Ser Lys Ala Thr
20 25 30
Glu Ala Gly Gly Gly Asn Pro Ser Gly Ile Tyr Ser Ala Ile Ile Ser
35 40 45
Arg Asn Phe Pro Ile Ile Gly Val Lys Glu Lys Thr Phe Glu Gln Leu
50 55 60
His Lys Lys Cys Leu Glu Lys Lys Val Leu Tyr Val Asp Pro Glu Phe
65 70 75 80
Pro Pro Asp Glu Thr Ser Leu Phe Tyr Ser Gln Lys Phe Pro Ile Gln
85 90 95
Phe Val Trp Lys Arg Pro Pro Glu Ile Cys Glu Asn Pro Arg Phe Ile
100 105 110
Ile Asp Gly Ala Asn Arg Thr Asp Ile Cys Gln Gly Glu Leu Gly Asp
115 120 125
Cys Trp Phe Leu Ala Ala Ile Ala Cys Leu Thr Leu Asn Gln His Leu
130 135 140
Leu Phe Arg Val Ile Pro His Asp Gln Ser Phe Ile Glu Asn Tyr Ala
145 150 155 160
Gly Ile Phe His Phe Gln Phe Trp Arg Tyr Gly Glu Trp Val Asp Val
165 170 175
Val Ile Asp Asp Cys Leu Pro Thr Tyr Asn Asn Gln Leu Val Phe Thr
180 185 190
Lys Ser Asn His Arg Asn Glu Phe Trp Ser Ala Leu Leu Glu Lys Ala
195 200 205
Tyr Ala Lys Leu His Gly Ser Tyr Glu Ala Leu Lys Gly Gly Asn Thr
210 215 220
Thr Glu Ala Met Glu Asp Phe Thr Gly Gly Val Ala Glu Phe Phe Glu
225 230 235 240

Ile Arg Asp Ala Pro Ser Asp Met Tyr Lys Ile Met Lys Lys Ala Ile
 245 250 255
 Glu Arg Gly Ser Leu Met Gly Cys Ser Ile Asp Asp Gly Thr Asn Met
 260 265 270
 Thr Tyr Gly Thr Ser Pro Ser Gly Leu Asn Met Gly Glu Leu Ile Ala
 275 280 285
 Arg Met Val Arg Asn Met Asp Asn Ser Leu Leu Gln Asp Ser Asp Leu
 290 295 300
 Asp Pro Arg Gly Ser Asp Glu Arg Pro Thr Arg Thr Ile Ile Pro Val
 305 310 315 320
 Gln Tyr Glu Thr Arg Met Ala Cys Gly Leu Val Arg Gly His Ala Tyr
 325 330 335
 Ser Val Thr Gly Leu Asp Glu Val Pro Phe Lys Gly Glu Lys Val Lys
 340 345 350
 Leu Val Arg Leu Arg Asn Pro Trp Gly Gln Val Glu Trp Asn Gly Ser
 355 360 365
 Trp Ser Asp Arg Trp Lys Asp Trp Ser Phe Val Asp Lys Asp Glu Lys
 370 375 380
 Ala Arg Leu Gln His Gln Val Thr Glu Asp Gly Glu Phe Trp Met Ser
 385 390 395 400
 Tyr Glu Asp Phe Ile Tyr His Phe Thr Lys Leu Glu Ile Cys Asn Leu
 405 410 415
 Thr Ala Asp Ala Leu Gln Ser Asp Lys Leu Gln Thr Trp Thr Val Ser
 420 425 430
 Val Asn Glu Gly Arg Trp Val Arg Gly Cys Ser Ala Gly Gly Cys Arg
 435 440 445
 Asn Phe Pro Asp Thr Phe Trp Thr Asn Pro Gln Tyr Arg Leu Lys Leu
 450 455 460
 Leu Glu Glu Asp Asp Asp Pro Asp Asp Ser Glu Val Ile Cys Ser Phe
 465 470 475 480
 Leu Val Ala Leu Met Gln Lys Asn Arg Arg Lys Asp Arg Lys Leu Gly
 485 490 495
 Ala Ser Leu Phe Thr Ile Gly Phe Ala Ile Tyr Glu Val Pro Lys Glu
 500 505 510
 Met His Gly Asn Lys Gln His Leu Gln Lys Asp Phe Phe Leu Tyr Asn
 515 520 525
 Ala Ser Lys Ala Arg Ser Lys Thr Tyr Ile Asn Met Arg Glu Val Ser
 530 535 540
 Gln Arg Phe Arg Leu Pro Pro Ser Glu Tyr Val Ile Val Pro Ser Thr
 545 550 555 560
 Tyr Glu Pro His Gln Glu Gly Glu Phe Ile Leu Arg Val Phe Ser Glu

sub
 C1

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:1..61
- (D) OTHER INFORMATION:/label= ALU

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:268..309
- (D) OTHER INFORMATION:/label= ALU
/note= "FIGURE 3 - RAT"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:310..328
- (D) OTHER INFORMATION:/label= ALU
/note= "FIGURE 3 - RAT"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:578..618
- (D) OTHER INFORMATION:/label= ALU
/note= "FIGURE 3 - RAT"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:619..653
- (D) OTHER INFORMATION:/label= ALU
/note= "FIGURE 3 - RAT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Pro Thr Val Ile Ser Pro Thr Val Ala Pro Arg Thr Gly Ala Glu
1 5 10 15
Pro Arg Ser Pro Gly Pro Val Pro His Pro Ala Gln Gly Lys Thr Thr
20 25 30
Glu Ala Gly Gly Gly His Pro Gly Gly Ile Tyr Ser Ala Ile Ile Ser
35 40 45
Arg Asn Phe Pro Ile Ile Gly Val Lys Glu Lys Thr Phe Glu Gln Leu
50 55 60
His Lys Lys Cys Leu Glu Lys Lys Val Leu Tyr Leu Asp Pro Glu Phe
65 70 75 80
Pro Pro Asp Glu Thr Ser Leu Phe Tyr Ser Gln Lys Phe Pro Ile Gln
85 90 95
Phe Val Trp Lys Arg Pro Pro Glu Ile Cys Glu Asn Pro Arg Phe Ile
100 105 110
Ile Gly Gly Ala Asn Arg Thr Asp Ile Cys Gln Gly Asp Leu Gly Asp
115 120 125
Cys Trp Leu Leu Ala Ala Ile Ala Cys Leu Thr Leu Asn Glu Arg Leu
130 135 140
Leu Phe Arg Val Ile Pro His Asp Gln Ser Phe Thr Glu Asn Tyr Ala
145 150 155 160

Sub
C1

Gly Ile Phe His Phe Gln Phe Trp Arg Tyr Gly Asp Trp Val Asp Val
165 170 175

Val Ile Asp Asp Cys Leu Pro Thr Tyr Asn Asn Gln Leu Val Phe Thr
180 185 190

Lys Ser Asn His Arg Asn Glu Phe Trp Ser Ala Leu Leu Glu Lys Ala
195 200 205

Tyr Ala Lys Leu His Gly Ser Tyr Glu Ala Leu Lys Gly Gly Asn Thr
210 215 220

Thr Glu Ala Met Glu Asp Phe Thr Gly Gly Val Thr Glu Phe Phe Glu
225 230 235 240

Ile Lys Asp Ala Pro Ser Asp Met Tyr Lys Ile Met Arg Lys Ala Ile
245 250 255

Glu Arg Gly Ser Leu Met Gly Cys Ser Ile Asp Asp Gly Thr Asn Met
260 265 270

Thr Tyr Gly Thr Ser Pro Ser Gly Leu Asn Met Gly Glu Leu Ile Ala
275 280 285

Arg Met Val Arg Asn Met Asp Asn Ser Leu Leu Arg Asp Ser Asp Leu
290 295 300

Asp Pro Arg Ala Ser Asp Asp Arg Pro Ser Arg Thr Ile Val Pro Val
305 310 315 320

Gln Tyr Glu Thr Arg Met Ala Cys Gly Leu Val Arg Gly His Ala Tyr
325 330 335

Ser Val Thr Gly Leu Glu Glu Ala Leu Phe Lys Gly Glu Lys Val Lys
340 345 350

Leu Val Arg Leu Arg Asn Pro Trp Gly Gln Val Glu Trp Asn Gly Ser
355 360 365

Trp Ser Asp Gly Trp Lys Asp Trp Ser Phe Val Asp Lys Asp Glu Lys
370 375 380

Ala Arg Leu Gln His Gln Val Thr Glu Asp Gly Glu Phe Trp Met Ser
385 390 395 400

Tyr Asp Asp Phe Val Tyr His Phe Thr Lys Leu Glu Ile Cys Asn Leu
405 410 415

Thr Ala Asp Ala Leu Glu Ser Asp Lys Leu Gln Thr Trp Thr Val Ser
420 425 430

Val Asn Glu Gly Arg Trp Val Arg Gly Cys Ser Ala Gly Gly Cys Arg
435 440 445

Asn Phe Pro Asp Thr Phe Trp Thr Asn Pro Gln Tyr Arg Leu Lys Leu
450 455 460

Leu Glu Glu Asp Asp Asp Pro Asp Asp Ser Glu Val Ile Cys Ser Phe
465 470 475 480

Sub
C1

Leu Val Ala Leu Met Gln Lys Asn Arg Arg Lys Asp Arg Lys Leu Gly
485 490 495

Ala Asn Leu Phe Thr Ile Gly Phe Ala Ile Tyr Glu Val Pro Lys Glu
500 505 510

Met His Gly Asn Lys Gln His Leu Gln Lys Asp Phe Phe Leu Tyr Asn
515 520 525

Ala Ser Lys Ala Arg Ser Lys Thr Tyr Ile Asn Met Arg Glu Val Ser
530 535 540

Gln Arg Phe Arg Leu Pro Pro Ser Glu Tyr Val Ile Val Pro Ser Thr
545 550 555 560

Tyr Glu Pro His Gln Glu Gly Glu Phe Ile Leu Arg Val Phe Ser Glu
565 570 575

Lys Arg Asn Leu Ser Glu Glu Ala Glu Asn Thr Ile Ser Val Asp Arg
580 585 590

Pro Val Lys Lys Lys Lys Asn Lys Pro Ile Ile Phe Val Ser Asp Arg
595 600 605

Ala Asn Ser Asn Lys Glu Leu Gly Val Asp Gln Glu Ala Glu Glu Gly
610 615 620

Lys Asp Lys Thr Gly Pro Asp Lys Gln Gly Glu Ser Pro Gln Pro Arg
625 630 635 640

Pro Gly His Thr Asp Gln Glu Ser Glu Glu Gln Gln Gln Phe Arg Asn
645 650 655

Ile Phe Arg Gln Ile Ala Gly Asp Asp Met Glu Ile Cys Ala Asp Glu
660 665 670

Leu Lys Asn Val Leu Asn Thr Val Val Asn Lys His Lys Asp Leu Lys
675 680 685

Thr Gln Gly Phe Thr Leu Glu Ser Cys Arg Ser Met Ile Ala Leu Met
690 695 700

Asp Thr Asp Gly Ser Gly Arg Leu Asn Leu Gln Glu Phe His His Leu
705 710 715 720

Trp Lys Lys Ile Lys Ala Trp Gln Lys Ile Phe Lys His Tyr Asp Thr
725 730 735

Asp His Ser Gly Thr Ile Asn Ser Tyr Glu Met Arg Asn Ala Val Asn
740 745 750

Asp Ala Gly Phe His Leu Asn Ser Gln Leu Tyr Asp Ile Ile Thr Met
755 760 765

Arg Tyr Ala Asp Lys His Met Asn Ile Asp Phe Asp Ser Phe Ile Cys
770 775 780

Cys Phe Val Arg Leu Glu Gly Met Phe Arg Ala Phe His Ala Phe Asp
785 790 795 800

Lys Asp Gly Asp Gly Ile Ile Lys Leu Asn Val Leu Glu Trp Leu Gln

805

810

815

Leu Thr Met Tyr Ala
820

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:1..61
- (D) OTHER INFORMATION:/label= ALU
/note= "FIGURE 3 - PIG"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:268..309
- (D) OTHER INFORMATION:/label= ALU
/note= "FIGURE 3 - PIG"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:310..328
- (D) OTHER INFORMATION:/label= ALU
/note= "FIGURE 3 - PIG"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:578..618
- (D) OTHER INFORMATION:/label= ALU
/note= "FIGURE 3 - PIG"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:619..653
- (D) OTHER INFORMATION:/label= ALI
/note= "FIGURE 3 - PIG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Pro Thr Val Ile Ser Ala Ser Val Ala Pro Arg Thr Ala Ala Glu
1 5 10 15
Pro Arg Ser Pro Gly Pro Val Pro His Pro Ala Gln Ser Lys Ala Thr
20 25 30
Glu Ala Gly Gly Gly Asn Pro Ser Gly Ile Tyr Ser Ala Ile Ile Ser
35 40 45
Arg Asn Phe Pro Ile Ile Gly Val Lys Glu Lys Thr Phe Glu Gln Leu
50 55 60

Sub
C1

His Lys Lys Cys Leu Glu Lys Lys Val Leu Tyr Val Asp Pro Glu Phe
65 70 75 80
Pro Pro Asp Glu Thr Ser Leu Phe Tyr Ser Gln Lys Phe Pro Ile Gln
85 90 95
Phe Val Trp Lys Arg Pro Pro Glu Ile Cys Glu Asn Pro Arg Phe Ile
100 105 110
Ile Asp Gly Ala Asn Arg Thr Asp Ile Cys Gln Gly Glu Leu Gly Asp
115 120 125
Cys Trp Phe Leu Ala Ala Ile Ala Cys Leu Thr Leu Asn Gln His Leu
130 135 140
Leu Phe Arg Val Ile Pro His Asp Gln Ser Phe Ile Glu Asn Tyr Ala
145 150 155 160
Gly Ile Phe His Phe Gln Phe Trp Arg Tyr Gly Glu Trp Val Asp Val
165 170 175
Val Ile Asp Asp Cys Leu Pro Thr Tyr Asn Asn Gln Leu Val Phe Thr
180 185 190
Lys Ser Asn His Arg Asn Glu Phe Trp Ser Ala Leu Leu Glu Lys Ala
195 200 205
Tyr Ala Lys Leu His Gly Ser Tyr Glu Ala Leu Lys Gly Gly Asn Thr
210 215 220
Thr Glu Ala Met Glu Asp Phe Thr Gly Gly Val Ala Glu Phe Phe Glu
225 230 235 240
Ile Arg Asp Ala Pro Ser Asp Met Tyr Lys Ile Met Lys Lys Ala Ile
245 250 255
Glu Arg Gly Ser Leu Met Gly Cys Ser Ile Asp Asp Gly Thr Asn Met
260 265 270
Thr Tyr Gly Thr Ser Pro Ser Gly Leu Asn Met Gly Asp Leu Ile Ala
275 280 285
Arg Met Val Arg Asn Met Glu Asn Ser Arg Leu Arg Asp Ser Ile Leu
290 295 300
Asp Pro Glu Val Ser Asp Asp Arg Pro Thr Arg Thr Ile Val Pro Val
305 310 315 320
Gln Phe Glu Thr Arg Met Ala Cys Gly Leu Val Arg Gly His Ala Tyr
325 330 335
Ser Val Thr Gly Leu Glu Glu Ala Leu Phe Lys Gly Glu Lys Val Lys
340 345 350
Leu Val Arg Leu Arg Asn Pro Trp Gly Gln Val Glu Trp Asn Gly Ser
355 360 365
Trp Ser Asp Ser Trp Lys Asp Trp Ser Phe Val Asp Lys Asp Glu Lys
370 375 380
Ala Arg Leu Gln His Gln Val Thr Glu Asp Gly Glu Phe Trp Met Ser

Sub
C1

385	390	395	400
Tyr Asp Asp Phe Ile Tyr His Phe Thr Lys Leu Glu Ile Cys Asn Leu	405	410	415
Thr Ala Asp Ala Leu Glu Ser Asp Lys Leu Gln Thr Trp Thr Val Ser	420	425	430
Val Asn Glu Gly Arg Trp Val Arg Gly Cys Ser Ala Gly Thr Gly Arg	435	440	445
Asn Phe Pro Asp Thr Phe Trp Thr Asn Pro Gln Tyr Arg Leu Lys Leu	450	455	460
Leu Glu Glu Asp Asp Asp Pro Asp Asp Ser Glu Val Ile Cys Ser Phe	465	470	475
Leu Val Ala Leu Met Gln Arg Asn Arg Arg Lys Asp Arg Lys Leu Gly	485	490	495
Ala Asn Leu Phe Thr Ile Gly Phe Ala Ile Tyr Glu Val Pro Lys Glu	500	505	510
Met His Gly Asn Lys Gln His Leu Gln Lys Asp Phe Phe Leu Tyr Asn	515	520	525
Ala Ser Lys Ala Arg Ser Arg Thr Tyr Ile Asn Met Arg Glu Val Ser	530	535	540
Glu Arg Phe Arg Leu Pro Pro Ser Glu Tyr Val Ile Val Pro Ser Thr	545	550	555
Tyr Glu Pro His Gln Glu Gly Glu Phe Met Leu Arg Val Phe Ser Glu	565	570	575
Lys Arg Lys Leu Ser Glu Glu Val Glu Asn Thr Ile Ser Val Asp Arg	580	585	590
Pro Val Arg Lys Lys Lys Thr Lys Pro Ile Ile Phe Val Ser Asp Arg	595	600	605
Ala Asn Ser Asn Lys Glu Leu Gly Val Asp Gln Glu Ser Glu Glu Gly	610	615	620
Gln Asp Lys Thr Ser Pro Asp Lys Gln Glu Lys Ser Pro Lys Pro Glu	625	630	635
Pro Ser Asn Thr Asp Gln Glu Ser Glu Glu Gln Gln Gln Phe Arg Asn	645	650	655
Ile Phe Lys Gln Ile Ala Gly Asp Asp Met Glu Ile Cys Ala Asp Glu	660	665	670
Leu Lys Lys Val Leu Asn Thr Val Val Asn Lys His Lys Asp Leu Lys	675	680	685
Thr His Gly Phe Thr Leu Glu Ser Cys Arg Ser Met Ile Ala Leu Met	690	695	700
Asp Thr Asp Gly Ser Gly Lys Leu Asn Leu Gln Glu Phe His His Leu	705	710	715
			720

Trp Asn Lys Ile Lys Ala Trp Gln Lys Ile Phe Lys His Tyr Asp Thr
 725 730 735
 Asp Gln Ser Gly Thr Ile Asn Ser Tyr Glu Met Arg Asn Ala Val Asn
 740 745 750
 Asp Ala Gly Phe His Leu Asn Asn Gln Leu Tyr Asp Ile Ile Thr Met
 755 760 765
 Arg Tyr Ala Asp Lys His Met Asn Ile Asp Phe Asp Ser Phe Ile Cys
 770 775 780
 Cys Phe Val Arg Leu Glu Gly Met Phe Arg Ala Phe His Ala Phe Asp
 785 790 795 800
 Lys Asp Gly Asp Gly Ile Ile Lys Leu Asn Val Leu Glu Trp Leu Gln
 805 810 815
 Leu Thr Met Tyr Ala
 820

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:1..61
- (D) OTHER INFORMATION:/label= ALU
/note= "FIGURE 3 - COW"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:268..309
- (D) OTHER INFORMATION:/label= ALU
/note= "FIGURE 3 - COW"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:310..328
- (D) OTHER INFORMATION:/label= ALU
/note= "FIGURE 3 - COW"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:578..618
- (D) OTHER INFORMATION:/label= ALU
/note= "FIGURE 3 - COW"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:619..653
- (D) OTHER INFORMATION:/label= ALU

/note= "FIGURE 3 - COW"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Met Pro Thr Val Ile Ser Ala Ser Val Ala Pro Arg Thr Ala Ala Glu
1 5 10 15
Pro Arg Ser Pro Gly Pro Val Pro His Pro Ala Gln Ser Lys Ala Thr
20 25 30
Glu Ala Gly Gly Gly Asn Pro Ser Gly Ile Tyr Ser Ala Ile Ile Ser
35 40 45
Arg Asn Phe Pro Ile Ile Gly Val Lys Glu Lys Thr Phe Glu Gln Leu
50 55 60
His Lys Lys Cys Leu Glu Lys Lys Val Leu Tyr Val Asp Pro Glu Phe
65 70 75 80
Pro Pro Asp Glu Thr Ser Leu Phe Tyr Ser Gln Lys Phe Pro Ile Gln
85 90 95
Phe Val Trp Lys Arg Pro Pro Glu Ile Cys Glu Asn Pro Arg Phe Ile
100 105 110
Ile Asp Gly Ala Asn Arg Thr Asp Ile Cys Gln Gly Glu Leu Gly Asp
115 120 125
Cys Trp Phe Leu Ala Ala Ile Ala Cys Leu Thr Leu Asn Gln His Leu
130 135 140
Leu Phe Arg Val Ile Pro His Asp Gln Ser Phe Ile Glu Asn Tyr Ala
145 150 155 160
Gly Ile Phe His Phe Gln Phe Trp Arg Tyr Gly Glu Trp Val Asp Val
165 170 175
Val Ile Asp Asp Cys Leu Pro Thr Tyr Asn Asn Gln Leu Val Phe Thr
180 185 190
Lys Ser Asn His Arg Asn Glu Phe Trp Ser Ala Leu Leu Glu Lys Ala
195 200 205
Tyr Ala Lys Leu His Gly Ser Tyr Glu Ala Leu Lys Gly Gly Asn Thr
210 215 220
Thr Glu Ala Met Glu Asp Phe Thr Gly Gly Val Ala Glu Phe Phe Glu
225 230 235 240
Ile Arg Asp Ala Pro Ser Asp Met Tyr Lys Ile Met Lys Lys Ala Ile
245 250 255
Glu Arg Gly Ser Leu Met Gly Cys Ser Ile Asp Asp Gly Thr Asn Met
260 265 270
Thr Tyr Gly Thr Ser Pro Ser Gly Leu Asn Met Gly Glu Leu Ile Glu
275 280 285
Arg Met Val Arg Asn Met Asp Asn Ser Arg Leu Arg Asp Ser Ile Leu
290 295 300

Sub
C1

Asp Pro Glu Val Ser Asp Asp Arg Pro Thr Arg Met Ile Val Pro Val
305 310 315 320
Gln Phe Glu Thr Arg Met Ala Cys Gly Leu Val Arg Gly His Ala Tyr
325 330 335
Ser Val Thr Gly Leu Glu Glu Ala Leu Tyr Lys Gly Glu Lys Val Lys
340 345 350
Leu Val Arg Leu Arg Asn Pro Trp Gly Gln Val Glu Trp Asn Gly Ser
355 360 365
Trp Ser Asp Ser Trp Lys Asp Trp Ser Tyr Val Asp Lys Asp Glu Lys
370 375 380
Ala Arg Leu Gln His Gln Val Thr Glu Asp Gly Glu Phe Trp Met Ser
385 390 395 400
Tyr Glu Asp Phe Ile Tyr His Phe Thr Lys Leu Glu Ile Cys Asn Leu
405 410 415
Thr Ala Asp Ala Leu Gln Ser Asp Lys Leu Gln Thr Trp Thr Val Ser
420 425 430
Val Asn Glu Gly Arg Trp Val Arg Gly Cys Ser Ala Gly Gly Cys Arg
435 440 445
Asn Phe Pro Asp Thr Phe Trp Thr Asn Pro Gln Tyr Arg Leu Lys Leu
450 455 460
Leu Glu Glu Asp Asp Asp Pro Asp Asp Ser Glu Val Ile Cys Ser Phe
465 470 475 480
Leu Val Ala Leu Met Gln Lys Asn Arg Arg Lys Asp Arg Lys Leu Gly
485 490 495
Ala Ser Leu Phe Thr Ile Gly Phe Ala Ile Tyr Glu Val Pro Lys Glu
500 505 510
Met His Gly Asn Lys Gln His Leu Gln Lys Asp Phe Phe Leu Tyr Asn
515 520 525
Ala Ser Lys Ala Arg Ser Lys Thr Tyr Ile Asn Met Arg Glu Val Ser
530 535 540
Gln Arg Phe Arg Leu Pro Pro Ser Glu Tyr Val Ile Val Pro Ser Thr
545 550 555 560
Tyr Glu Pro His Gln Glu Gly Glu Phe Ile Leu Arg Val Phe Ser Glu
565 570 575
Lys Arg Asn Leu Ser Glu Glu Val Glu Asn Thr Ile Ser Val Asp Arg
580 585 590
Pro Val Lys Lys Lys Lys Thr Lys Pro Ile Ile Phe Val Ser Asp Arg
595 600 605
Ala Asn Ser Asn Lys Glu Leu Gly Val Asp Gln Glu Ser Glu Glu Gly
610 615 620

Lys Gly Lys Thr Ser Pro Asp Lys Gln Lys Gln Ser Pro Gln Pro Gln
 625 630 635 640
 Pro Gly Ser Ser Asp Gln Glu Ser Glu Glu Gln Gln Gln Phe Arg Asn
 645 650 655
 Ile Phe Lys Gln Ile Ala Gly Asp Asp Met Glu Ile Cys Ala Asp Glu
 660 665 670
 Leu Lys Lys Val Leu Asn Thr Val Val Asn Lys His Lys Asp Leu Lys
 675 680 685
 Thr His Gly Phe Thr Leu Glu Ser Cys Arg Ser Met Ile Ala Leu Met
 690 695 700
 Asp Thr Asp Gly Ser Gly Lys Leu Asn Leu Gln Glu Phe His His Leu
 705 710 715 720
 Trp Asn Lys Ile Lys Ala Trp Gln Lys Ile Phe Lys His Tyr Asp Thr
 725 730 735
 Asp Gln Ser Gly Thr Ile Asn Ser Tyr Glu Met Arg Asn Ala Val Asn
 740 745 750
 Asp Ala Gly Phe His Leu Asn Asn Gln Leu Tyr Asp Ile Ile Thr Met
 755 760 765
 Arg Tyr Ala Asp Lys His Met Asn Ile Asp Phe Asp Ser Phe Ile Cys
 770 775 780
 Cys Phe Val Arg Leu Glu Gly Met Phe Arg Ala Phe His Ala Phe Asp
 785 790 795 800
 Lys Asp Gly Asp Gly Ile Ile Lys Leu Asn Val Leu Glu Trp Leu Gln
 805 810 815
 Leu Thr Met Tyr Ala
 820

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (D) OTHER INFORMATION: /label= Table 1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

ATGGAGCCAA CAGAACTGAC

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Primer

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION: /label= Table 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GTATGACTCG GAAAAGAAGGT

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Primer

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION: /label= Table 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TAAGCAAAAG CAGTCCCCAC

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION: /label= Table 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TTGCTGTTCC TCACTTTCCTG

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= Table 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GTTTCATCTG CTGCTTCGTT

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= Table 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTGGTTCAGG CATACTGGT

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= Table 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TTCTTTATGT GGACCCTGAG TT

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= Table 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ACGAACTGGA TGGGGAAC

(2) INFORMATION FOR SEQ ID NO:18 :

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

- (ix) FEATURE:
(A) NAME/KEY: misc feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTCAGTACCTCCCGTTCACC

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

- (ix) FEATURE:
(A) NAME/KEY: misc feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATGCTTGAGCCAGGAAAAC

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

- (ix) FEATURE:
(A) NAME/KEY: misc feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTTTCCTTGAAGGTAGCTGTAT

(2) INFORMATION FOR SEQ ID NO:21 :

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21 :

GAGGTGCTGAGTGAGAGGAC

(2) INFORMATION FOR SEQ ID NO:22 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22 :

ACTCCGTCTCAAAAAATACCT

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23 :

ATTGTCCCTTTACCTCCTGG

(2) INFORMATION FOR SEQ ID NO:24 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24 :

TGGAAGTAGGAGAGTGGGCA

(2) INFORMATION FOR SEQ ID NO:25 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:
(A) NAME/KEY: misc feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25 :

GGGTAGATGGGTGGGAAGTT

(2) INFORMATION FOR SEQ ID NO:26 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:
(A) NAME/KEY: misc feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26 :

GAGGAATGTGGAGGAAGGAC

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:
(A) NAME/KEY: misc feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTCCTGTGAGTGAGGTCTCG

(2) INFORMATION FOR SEQ ID NO:28 :

Sub
C1

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28 :

GGAACTCTGTGACCCCAAAT

(2) INFORMATION FOR SEQ ID NO:29 :

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29 :

TCCTCAAACAAAACATTTCGC

(2) INFORMATION FOR SEQ ID NO:30 :

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTTCCCTACATTCTCCATCG

(2) INFORMATION FOR SEQ ID NO:31 :

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

Sub
C1

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31 :

GTTATTTCAACCCAGACCCTT

(2) INFORMATION FOR SEQ ID NO:32 :

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32 :

AATGGGTTCTCTGGTTACTGC

(2) INFORMATION FOR SEQ ID NO:33 :

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33 :

AGCACGAAAAGCAAAGATAAA

(2) INFORMATION FOR SEQ ID NO:34 :

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34 :

Sub
C1

GTAAGAGATTTGCCCCCAG

(2) INFORMATION FOR SEQ ID NO:35 :

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35 :

TCTGCGGATCATTGGTTTTG

(2) INFORMATION FOR SEQ ID NO:36 :

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36 :

CCTTCCCTTCTTCTGCTTC

(2) INFORMATION FOR SEQ ID NO:37 :

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37 :

CTCTCTTCCCCACCCTTACC

(2) INFORMATION FOR SEQ ID NO:38 :

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid

Sub
C1

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38 :

CCTCCTCACCTGCTCCATA

(2) INFORMATION FOR SEQ ID NO:39 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39 :

TTTTTCGGCTTAGACCTCC

(2) INFORMATION FOR SEQ ID NO:40 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40 :

TGTGGGAATAGAAATAATGG

(2) INFORMATION FOR SEQ ID NO:41 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41 :

CCAGGAGCTCTGTGGGTCA

(2) INFORMATION FOR SEQ ID NO:42 :

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42 :

GGCTCCTCATCCTCATTCACA

(2) INFORMATION FOR SEQ ID NO:43 :

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GTGGAGGAGGGTGAGTGTGC

(2) INFORMATION FOR SEQ ID NO:44 :

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44 :

TGTGGCAGGACAGGACGTTC

(2) INFORMATION FOR SEQ ID NO:45 :

Sub
C1

- Sub
C1
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45 :

TTCAACCTCTGGAGTGGGCC

(2) INFORMATION FOR SEQ ID NO:46 :

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46 :

CACCAGAGCAAACCGTCCAC

(2) INFORMATION FOR SEQ ID NO:47 :

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47 :

ACAGCCCAGACTCCCATTCC

(2) INFORMATION FOR SEQ ID NO:48 :

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48 :

TTCTCTTCTCCCTTCACCCCT

(2) INFORMATION FOR SEQ ID NO:49 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49 :

ACACACTTCATGCTCTCTACCC

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50 :

CCGCCTATTCCCTTCCTCTT

(2) INFORMATION FOR SEQ ID NO:51 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51 :

GACAAACTCCTGGGAAGCCT

(2) INFORMATION FOR SEQ ID NO:52 :

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52 :

ACCTCTGACCCCTGTGAACC

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53 :

TGTGGATTTGTGTGCTACGC

(2) INFORMATION FOR SEQ ID NO:54 :

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54 :

CATAAATAGCACCGACAGGGA

(2) INFORMATION FOR SEQ ID NO:55 :

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

Sub
C1

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

(A) NAME/KEY: misc feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55 :

GGGATGGAGAAGAGTGAGGA

(2) INFORMATION FOR SEQ ID NO:56 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

(A) NAME/KEY: misc feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56 :

TCCTCACTCTTCTCCATCCC

(2) INFORMATION FOR SEQ ID NO:57 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

(A) NAME/KEY: misc feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57 :

ACCCTGTATGTTGCCTTGG

(2) INFORMATION FOR SEQ ID NO:58 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58 :

GGGGATTTTGCTGTGTGCTG

(2) INFORMATION FOR SEQ ID NO:59 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59 :

ATTCCTGCTCCCACCGTCTC

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60 :

CACAGAGTGTCCGAGAGGCA

(2) INFORMATION FOR SEQ ID NO:61 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61 :

GGAGATTATCAGGTGAGATGCC

(2) INFORMATION FOR SEQ ID NO:62 :

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62 :

CAGAGTGTCCGAGAGGCAGGG

(2) INFORMATION FOR SEQ ID NO:63 :

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63 :

CGTTGACCCCTCCACCTTGA

(2) INFORMATION FOR SEQ ID NO:64 :

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64 :

GGGAAAAACATGCACCTTCTT

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

(A) NAME/KEY: misc feature

(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65 :

TAGGGGGTAAAAATGGAGGAG

(2) INFORMATION FOR SEQ ID NO:66 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

(A) NAME/KEY: misc feature

(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66 :

ACTAACTCAGTGGAATAGGG

(2) INFORMATION FOR SEQ ID NO:67 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(ix) FEATURE:

(A) NAME/KEY: misc feature

(D) OTHER INFORMATION:/label= Table 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67 :

GGAGCTAGGATAGCTCAAT

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